

SEQUENCE LISTING

<110> Lukyanov, Sergey

<120> FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING SAME
<130> U 015759-8

<140> 10/533,781

<141> 2005-05-04

<160> 28

<170> PatentIn version 3.1

<210>. 1

<211> 1010

<212> DNA

<213> Pontellina plumata

<400> 1

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tccctgagca gggacgtatg accaacaaga tgaagtctac caagggcgcc ttgaccttct	180
ccccctaccc tctctctcat gtcatggat acgggttcta ccactttggg acctatccc	240
gtgggtatga gaatcccttc ctgcattGCCG ccaacaacgg ggggtacacc aacaccagga	300
ttgagaagta tgaggatgga ggagttcttc atgttagctt cagctacaga tatgaagcag	360
gcagggttat tggggatttc aagggtgtcg ggacaggatt ccctgaggac agtgtatct	420
tcaccgacaa gatcatccgg tccaatgcta ccgtggagca cttgcaccca atggagaca	480
acgttcttgt gggctccttc gcgagaacct tttccctgag ggatggaggc tactactcat	540
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gggggtccat gttgccttc aggagagttg aggaacttca ctccaaacact gaacttggca	660
ttgttagagta tcaacatgcc ttcaagactc ccacagcatt tgcctgaact agaaaagtatc	720
aaatataaaac agagtacaa aggatctgtc gtcattctaa actttgtatg atttacaaat	780
aatgatttaa tggcaactcc caaaatagac ttgaattaat tgaaaaatca actaaacata	840
atccttggtg ctctgttgat atgaacgctt tctgacttgg accccggctt gaactgaccc	900
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<210> 2

<211> 222

<212> PRT

<213> Pontellina plumata

<400> 2

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 Val Val Phe Glu Leu Val Gly Gly Gly Glu Gly Ile Pro Glu Gln Gly
 20 25 30
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Ser Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 3

<211> 1010

<212> DNA

<213> Pontellina plumata

<400> 3

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ctcctgagca gggacgtatg accaacaaga tgaagtctac caagggcgcc ttgaccttct	180
ccccctacct tctctctcat gtcatggat acgggttcta ccacttttgtt acctatccca	240
gtgggtatga gaatcccttc ctgcatgcc a tcaacaacgg ggggtacacc aacaccagga	300

ttgagaagta tgaggatgga ggagttcttc atgttagctt tagctacaga tatgaagcag 360
 gcagggtgat tggggatttc aaggttgtcg ggacaggatt ccctgaggac agtgtgatct 420
 tcaccgacaa gatcatccgg tccaatgcta ccgtggagca cttgcaccca atgggagaca 480
 acgttcttgtt gggctccttc gcgagaacct tttccctgag gcatggaggc tactactcat 540
 ttgtgggtga cagccacatg cacttcaaga gtgccatcca cccatccatc ctccagaacg 600
 gggggcccat gtttgccttc aggagagttg aggaacttca ctccaacact gaacttggca 660
 ttgttagagta tcaacatgcc ttcaagactc ccatagcatt tgcttaaact acaaagtatc 720
 aaatattaac agattgacaa aggatatgtc gtcattctaa actttgtatg atttacaaat 780
 aatgatttaa tgtcaaccct caaaaataggc ttgaattaat tgaaaaatca actaaacata 840
 atccttggtg ctctgttcat atgaacactt tctgacttgg accccggctt gaactgaccc 900
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<210> 4

<211> 222

<212> PRT

<213> Pontellina plumata

<400> 4

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									25						30
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
									35						45
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
									50						60
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
									65						80
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
									85						95
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
									100						110
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
									115						125
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
									130						140
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
									145						160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
									165						175

Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205

Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
 210 215 220

<210> 5
 <211> 814
 <212> DNA
 <213> *Labidocera aestiva*
 <400> 5

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 attgagtgcc gtatctctgg aaccatgaac ggagaggagt tttagcttgtt aggagctggc 120
 gatggaaaca ctgatgaagg acgtatgacc aacaagatga agtccaccaa aggacctctc 180
 tccttctctc cctacctact ctcccacatc atgggctacg gattcttatca ctatgctacc 240
 ttccctgctg gatatgagaa tgtctacctc catgctgcta agaatggagg ctacaccaac 300
 accaggactg agaggtacga agacggagga atcatttcgg tcaacttcac ctacagatat 360
 gagggaaaca aggttatcgg agactcaag gttgttggat caggattccc agctaacagt 420
 gttatcttca ctgacaagat catcaagtcc aacccaacct gtgagcacat ctaccccaag 480
 ggagataata ttcttgcata tgcctacact cgaacttgga tgctgagaga tggtgatac 540
 tactctgcac aggtcaacaa tcatactccac ttcaagactg ccatgcatcc caccatgctc 600
 cagaacggag gatccatgtt tacctacagg aagggttggagg agctccacag ccagtcagat 660
 gttgttattg tagaatacca acatgttttc aagaccccaa ctgctttgc ctaagcttgg 720
 aaatatggtt cctatcagac aattaataca ataaacttta cttatcattt taaaacccaa 780
 ctcttttaat gaataaattt ctgtatctac tact 814

<210> 6
 <211> 222
 <212> PRT
 <213> *Labidocera aestiva*
 <400> 6

Met Pro Val Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
 1 5 10 15
 Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
 20 25 30
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
 35 40 45

Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala
 50 55 60
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn
 65 70 75 80

 Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
 85 90 95
 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
 130 135 140
 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe
 165 170 175
 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 7
 <211> 753
 <212> DNA
 <213> cf. Pontella meadi Wheeler
 <400> 7

atcagttcat cagtacacga gcagagtcac acatcaaaat gcctgacatg aagcttgagt	60
gccacatctc cggaaccatg aatggagagg agtttgaact tattggtgct ggagatggaa	120
atacagatga gggacgcatg accaacaaaa tgaagtccat caaaggacct atctccttct	180
ctccctacct cctctcccac attcttggct acggatatta ccactttgca accttccttg	240
ctggatatga aaatatctac cttcatgcca tgaagaatgg aggttactcc aatgtcagaa	300
ctgagaggta tgaggatgga ggcatcattt ctataaccctt caactacaga tatgaaggga	360
acaagatcat tggagacttc aagggttgttga acaggatt ccctaccaac agtcttatct	420
tcactgacaa gatcattaaa tccaacccta cctgtgagaa catgttcccc aaggctgaca	480
atactcttgt gaatgcctac accagaacat atttgcttaa agatggtgga tactactctg	540
cccaggttaa caaccatatg cacttcaaga gtgccatcca taccaccatg ctccagaatg	600
gcggatccat gttcacctac agagttgttag aggagacaca cactcagaac gaagttgcta	660

ttgttagagta ccaaaatgtc ttcaaaaactc caactgcgtt tgcttgaaat acttgtaata	720
aaactgcaaa gaaataaaact aaattgtaca atc	753

<210> 8
<211> 222
<212> PRT
<213> cf. Pontella meadi Wheeler
<400> 8

Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly			
1	5	10	15
Glu Glu Phe Glu Leu Ile Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly			
20	25	30	
Arg Met Thr Asn Lys Met Lys Ser Ile Lys Gly Pro Ile Ser Phe Ser			
35	40	45	
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala			
50	55	60	
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn			
65	70	75	80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile			
85	90	95	
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Asn Lys Ile Ile Gly			
100	105	110	
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Thr Asn Ser Leu Ile Phe			
115	120	125	
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro			
130	135	140	
Lys Ala Asp Asn Thr Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu			
145	150	155	160
Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe			
165	170	175	
Lys Ser Ala Ile His Thr Thr Met Leu Gln Asn Gly Gly Ser Met Phe			
180	185	190	
Thr Tyr Arg Val Val Glu Glu Thr His Thr Gln Asn Glu Val Ala Ile			
195	200	205	
Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala			
210	215	220	

<210> 9
<211> 880
<212> DNA

<213> cf. Pontella meadi Wheeler

<400> 9

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tcaaaatgcc tgacatgaag cttgagtgcc acatctccgg aaccatgaat ggagaggagt	180
ttgaacttat tggttctgga gatggaaata ctgatcaggg acgcatgaca aacaatatga	240
agtccatcaa aggacctc tccttctc cctacctact ctcccacatt ctggctatg	300
gatattacca cttgcaacc ttccctgctg gatatgaaaa tatctacatt catgccatga	360
agaatggagg ttactcaa at gtcaggactg agaggatga ggtatggagc atcattcta	420
taaccttcaa ctacagatat gaaggcagca agatcattgg agacttcaaa gttattggaa	480
caggattccc taccgacagt cttatcttca ctgacaagat cattaaatcc aaccctacct	540
gcgagaacat gttccccaaag gctgacaaca ttcttgtgaa tgcctacacc agaacctatt	600
tgcttaaaga tggtgatac tactctgccc aggttaacaa ccatatgcac ttcaagagt	660
ccatccatcc tacaatgctc cagaatggtg gatccatgtt cactcacaga gtagtagagg	720
agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtctc aaaactccta	780
ctgcatttgc ttaaaaact tgotaacaaaa ctgcaaagaa ataacctata ttgtacaata	840
gcattttatt aatgcataaga aaaataaatg tatatttat	880

<210> 10

<211> 222

<212> PRT

<213> cf. Pontella meadi Wheeler

<400> 10

Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly			
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Glu Glu Phe Glu Leu Ile Gly Ser Gly Asp Gly Asn Thr Asp Gln Gly			
20	25	30	
Arg Met Thr Asn Asn Met Lys Ser Ile Lys Gly Pro Leu Ser Phe Ser			
35	40	45	
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala			
50	55	60	
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn			
65	70	75	80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile			
85	90	95	
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly			
100	105	110	
Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe			
115	120	125	

Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
 130 135 140
 Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
 145 150 155 160

 Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr His Arg Val Val Glu Glu Asn His Thr Lys Thr Asn Val Ala Ile
 195 200 205
 Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 11

<211> 847

<212> DNA

<213> Pontella mediterranea

<400> 11

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tttgaacttg ttggtgctgg agaaggaaac actgatgagg gacgcatgac caacaagatg	180
aagtccacca agggacctct ttccttctct ccttatttgc tctcccacgt tcttggttat	240
ggatactacc actatgctac ctccccgtct ggatatgaaa atgtctacct ccatgccatg	300
aagaatggag gttactccaa cacaagaact gagaggtatg aggatggagg tatcatttct	360
gctacccatca actacagata tgaagggaga cagattcatg gagacttcaa ggttgttagga	420
acgggattcc ctgccgacag catcatcttc actgacaaga tcatacgatc caaccctacc	480
tgtgagcaca tctaccccaa ggctaacaat attcttgta atgcttacac cagaacctgg	540
atgcttagag atggtgata ctactctgcc caggtcaaca accacatgca tttacagagt	600
gccattcatc ccaccatgct caagaatggt ggatctatgt tcacccatag aaaggttgag	660
gagctccaca cacaactga agtcggattt gttgaataacc agcatgtctt caagaggcca	720
actgcttttg cttaattttg taaataaaga aagaatctat aatgcaatag taccttaaag	780
ttttcaggat aataaatata taaagattt taataaaaaaa aaaaaaaaaa aaaaaaaaaa	840
aaaaaaaa	847

<210> 12

<211> 222

<212> PRT

<213> Pontella mediterranea

<400> 12

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									20			25			30
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Pro	Leu	Ser	Phe	Ser
									35			40			45
Pro	Tyr	Leu	Leu	Ser	His	Val	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Tyr	Ala
									50			55			60
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Val	Tyr	Leu	His	Ala	Met	Lys	Asn
									65			70			75
Gly	Gly	Tyr	Ser	Asn	Thr	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
									85			90			95
Ile	Ser	Ala	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Arg	Gln	Ile	His	Gly
									100			105			110
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Ala	Asp	Ser	Ile	Ile	Phe
									115			120			125
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	His	Ile	Tyr	Pro
									130			135			140
Lys	Ala	Asn	Asn	Ile	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Trp	Met	Leu
									145			150			155
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Leu
									165			170			175
Gln	Ser	Ala	Ile	His	Pro	Thr	Met	Leu	Lys	Asn	Gly	Gly	Ser	Met	Phe
									180			185			190
Thr	Tyr	Arg	Lys	Val	Glu	Glu	Leu	His	Thr	Gln	Thr	Glu	Val	Gly	Ile
									195			200			205
Val	Glu	Tyr	Gln	His	Val	Phe	Lys	Arg	Pro	Thr	Ala	Phe	Ala		
									210			215			220

<210> 13

<211> 850

<212> DNA

<213> Pontella mediterranea

<400> 13

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tttgaacttg ttgggtgctgg agatggaaac actgatgagg gacgcacatgac caaccagatg 180
aagtccaccaa agggacacct ctccctctct ccctacttgc tctcccacgt tcttgctat 240
ggataactacc actatgctac ctccctgct ggatatgaaa atgtctaccc ccatgccatg 300

aagaatggag gttactccaa cacaagaact gagaggtatg acgatggagg tatcatttct	360
gctaccttca actacagata tgaaggaga cagattcatg gagacttcaa ggttgttggaa	420
actggattcc ctgccgacag catcatcttc actgacaaga tcatcaagtc caaccctacc	480
tgtgagcaca tctaccccaa ggctgacaat attcttgtga atgcctacac cagaacctgg	540
atgcttagag atggtgata ctactctgct caggtcaaca accacatgca ctttaagagt	600
gccatccatc ccaccatgct ccagaatggt ggatctatgt tcacctacag aaaggtttag	660
gagctccaca cacaaactga agttggattt gttgagtacc agcatgtttt caagaggccc	720
acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgctttatg	780
tttctaaaac aatgaatgta taaataaatc tcaaaatatt caaaaaaaaaaaaaaaa	840
aaaaaaaaaaa	850

<210> 14
<211> 222
<212> PRT
<213> Pontella mediterranea
<400> 14

Met Pro His Met Lys Leu Glu Cys Arg Ile Ser Gly Thr Met Asn Gly			
1	5	10	15
Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly			
20	25	30	
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser			
35	40	45	
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala			
50	55	60	
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn			
65	70	75	80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile			
85	90	95	
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly			
100	105	110	
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe			
115	120	125	
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro			
130	135	140	
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu			
145	150	155	160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe			
165	170	175	
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe			
180	185	190	

Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
 210 215 220

<210> 15

<211> 821

<212> DNA

<213> Unknown

<220>

<223> nucleic acid sequence for pdae1GFP from an unidentified
 Pontellidae species, complete cds

<400> 15

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ggaaataactg atcagggacg tatgaccaac aagatgaaat ctaccaaggg tccactctcc	180
ttctctccct atcttctctc tcatgtcatg ggatATggat tctatcattt tgAACACATT	240
cccagtggTT atgagaatcc ctatgtccac gccatgacga acggTggata taccaacacc	300
aggattgaaa gttatgaaga tggagggttt cttaaccta cttcaacta cagattggat	360
ggaaacaaga ttatcgggGA cttcaagtgt gtcggAACtG gattccCTGA ggacAGCGTT	420
atcttcactg acaagatcat caagtccAAc cccatttGTG aacatttcta tccaatggct	480
aaaaacatca tgaaaaatgc ctacatgaga actctctccc tcagagatgg tggctactac	540
tctggccagg ttaccagCCA catccacttc aagaatgcGA tccacccATC catcCTTCat	600
aacggcggat ccatgttCAC ctacagaaga gttgaggAGC tccacactCA aactgatCTT	660
ggaattttTG agtaccAGCA tgtattcaag actcccACTG ctTTGCTTg aatGCCatGA	720
agatgaaACC tgaacaAGAT caatcttAT ttaccacaAT atgtAAATTG ttAAATTGTA	780
taattctcGA gaattcatAT aatacatAGA atttatCTTA C	821

<210> 16

<211> 222

<212> PRT

<213> Unknown

<220>

<223> amino acid sequence for pdae1GFP from an unidentified Pontellidae
 species

<400> 16

Met Ala Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Met Asn Gly			
1	5	10	15
Val Glu Phe Glu Leu Val Gly Gly Glu Gly Asn Thr Asp Gln Gly			

20

25

30

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly
 100 105 110
 Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro
 130 135 140
 Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe
 165 170 175
 Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 17

<211> 669

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the humanized version of the ppluGFP2
<400> 17

atgcccggcca tgaagatcga gtgccgcattc accggcaccc tgaacggcggt ggagttcgag	60
ctgggtggcg gcggagaggg caccggcgag cagggccgca tgaccaacaa gatgaagagc	120
accaaggcgcc ccctgacctt cagccccctac ctgctgagcc acgtgtatggg ctacggcttc	180
taccacttcg gcacacctacc cagcggctac gagaacccct tcctgcacgc catcaacaac	240
ggcggctaca ccaacaccccg catcgagaag tacggaggacg gcggcggtgct gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtgggt gggcacccggc	360
ttccccggagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag	420

cacctgcacc ccatggcga taacgtgctg gtgggcagct tcgcccgcac cttagccctg 480
 cgcgacggcg gctactacag ctgcgtggtg gacagccaca tgcaattcaa gagcgccatc 540
 caccccgca tcctgcagaa cgggggcccc atgttcgcct tccgcccgt ggaggagctg 600
 cacagcaaca ccgagctggg catcggtgg taccagcacg cttcaagac cccgatcgca 660
 ttgcctga 669
 <210> 18
 <211> 222
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> amino acid sequence for the humanized version of the ppluGFP2
 <400> 18

Met	Pro	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Leu	Asn	Gly
1									10					15	
Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly
									25					30	
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
									35					45	
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
							50		55				60		
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
						65		70			75			80	
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
							85		90				95		
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
						100		105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
						115		120					125		
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
						130		135			140				
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
						145		150			155			160	
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
							165		170				175		
Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Gly	Pro	Met	Phe
							180		185				190		
Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	Ser	Asn	Thr	Glu	Leu	Gly	Ile
							195		200			205			
Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr	Pro	Ile	Ala	Phe	Ala		
							210		215			220			

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<210> 19
<211> 589
<212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the ppluGFP2 with yeast-optimized codon
      usage
<400> 19
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tactccagaa	caaggttagaa	tgactaataa	aatgaaatct	actaaaggta	ctttgacttt	60
ttctccatat	tttgtgtctc	atgttatggg	ttatggtttt	tatcattttgc	gtacttatcc	120
atctggttat	gaaaatccat	ttttgcatttc	tattaataat	gggggttata	ctaatactag	180
aattgaaaaaa	tatgaagatg	gtgggttttt	gcatgtttct	ttttcttata	gatatgaagc	240
tggtagagtt	attggcgatt	ttaaagtgtt	tggtactgg	tttccagaag	attctgttat	300
ttttactgat	aaaattatta	gatctaatttc	tactgttcaa	catttgcattc	caatgggtga	360
taatgttttgc	gttgggtctt	ttgctagaac	ttttcttgc	agagatgg	gttattattc	420
ttttgttgc	gattctcata	tgcattttaa	atctgttatt	catccatcta	ttttgaaaaa	480
tggtggtcca	atgtttgctt	ttagaagagt	tgaagaatttgc	cattctata	ctgaatttggg	540
tattgttgc	atatcaacatg	cttttaaaac	tccaaatttgc	tttgctttaa		589

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<210> 20
<211> 222
<212> PRT
<213> Artificial sequence
<220>
<223> amino acid sequence for the ppluGFP2 with yeast-optimized codon u
      sage
<400> 20
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Met	Pro	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Leu	Asn	Gly	
1				5					10					15		
Val	Glu	Phe	Glu	Lys	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly
						20				25				30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser	
							35				40			45		
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly	
							50			55			60			
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn	
							65			70			75		80	
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val	

85	90	95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly		
100	105	110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe		
115	120	125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro		
130	135	140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu		
145	150	155
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe		
165	170	175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe		
180	185	190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile		
195	200	205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala		
210	215	220

<210> 21
 <211> 669
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> nucleic acid sequence for the CopCFP mutant
 <400> 21

atgcccggcca tgaagatcga gtgccgcatt accggcaccc tgaacggcgt ggagttcgag	60
ctgggtggcgc gcggagaggg caccggcag cagggccgca tgaccaacaa gatgaagagc	120
accaaaggcg ccctgacctt cagccccatc ctgctgagcc acgtgatggg ctggggcttt	180
taccacttcg gcacacctacc cagcggctac gagaacccct tcctgcacgc catcaacaac	240
ggcggctaca ccaacaccccg catcgagaag tacgaggacg gcccgtgt gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggg gggcaccggc	360
ttccccgagg acagcgtgat cttcaccgc aagatcatcc gcagcaacgc caccgtggag	420
cacctgcgcc ccatggcga taacgtgctg gtgggcagct tcggccgcac cttcagcctg	480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagccatc	540
caccccgagca tcctgcagaa cgggggcccc atgttcgcct tccggccgt ggaggagctg	600
cacagcaaca ccgagctggg catcgtggag taccagcacg cttcaagac cccgaccgca	660
ttcgcctaa	669

<210> 22
 <211> 222

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<212> PRT
<213> Artificial sequence
<220>
<223> amino acid sequence for the CopCFP mutant
<400> 22

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1 5 10 15
Val Glu Phe Glu Leu Val Gly Gly Glu Gly Thr Pro Glu Gln Gly
20 25 30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35 40 45
Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
50 55 60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65 70 75 80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85 90 95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100 105 110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115 120 125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
130 135 140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145 150 155 160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165 170 175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180 185 190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195 200 205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
210 215 220

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<210> 23
<211> 690
<212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the CopGFP-NA1 variant
<400> 23

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atggagagcg acgagagcgg cctgccgc	atggagatcg agtccgc	caccggcacc	60
ctgaacggcg tggagttcg	gctgggtggc ggcggagagg	gcaccccg	120
atgaccaaca agatgaagag	acccaagggc	gcctgac	180
cacgtatgg gctacggctt	ctaccacttc	ggcacctacc	240
ttccctgcac	ccatcaacaa	cgccggctac	300
ggcggcgtgc	tgcacgtgag	cttcagctac	360
ttcaagggtgg	tggcaccgg	cgctacgagg	420
cgcagcaac	ccaccgtgga	ccggccgcgt	480
ttcgccccca	ccttcagcct	gatcggcgac	540
atgcacttca	agagcgccat	tttcaccga	600
ttccggccgc	tgaggagct	caagatcatc	660
gccttcaaga	ccccgatcgc	cgacagccac	690

<210> 24
 <211> 229
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> amino acid sequence for the CopGFP-NA1 variant
 <400> 24

Met	Glu	Ser	Asp	Glu	Ser	Gly	Leu	Pro	Ala	Met	Glu	Ile	Glu	Cys	Arg
1															15
Ile	Thr	Gly	Thr	Leu	Asn	Gly	Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	
															20
															25
															30
Glu	Gly	Thr	Pro	Glu	Gln	Gly	Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr
															35
															40
															45
Lys	Gly	Ala	Leu	Thr	Phe	Ser	Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly
															50
															55
															60
Tyr	Gly	Phe	Tyr	His	Phe	Gly	Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro
															65
															70
															75
															80
Phe	Leu	His	Ala	Ile	Asn	Asn	Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu
															85
															90
															95
Lys	Tyr	Glu	Asp	Gly	Gly	Val	Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr
															100
															105
															110
Glu	Ala	Gly	Arg	Val	Ile	Gly	Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe
															115
															120
															125
Pro	Glu	Asp	Ser	Val	Ile	Phe	Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala
															130
															135
															140
Thr	Val	Glu	His	Leu	His	Pro	Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser

145	150	155	160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val			
165	170	175	
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu			
180	185	190	
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His			
195	200	205	
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr			
210	215	220	

Pro Ile Ala Phe Ala

225

<210> 25

<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

<400> 25

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ctgggtggcg gcggagaggg cacccccc gag cagggccgca tgaccaacaa gatgaagagc	120
accaaggcgcc ccctgacctt cagcccc tac ctgctgagcc acgtgatggg ctacggcttc	180
taccacttcg gcacaccttcc cagcggtac gagaacccct tcctgcacgc catcaacaac	240
ggcggctaca ccaacaccccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc	300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaagggtgtt gggcacccggc	360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag	420
cacctgcacc ccatggcgta taacgtgctg gtggcagct tcggccgcac cttcagccctg	480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc	540
caccccgacca tcctgcagaa cgggggcccc atgttcgcct tcggccgcgt ggaggagctg	600
cacagcaaca ccgagctggg catcggtgg taccagcacg cttcaagac cccgatcgca	660
ttcgccagat ccagagccca ggccagcaac tccgcccgtgg atggcacagc cggaccggga	720
tcggccgcga ctctagatca taatcagcca taccacattt gttagaggtt tacttgctt	780
aaaaaacctc ccacacctcc ccctgaacct gaaacataaa	819

<210> 26

<211> 272

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA2 variant

<400> 26

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Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Glu	Gly	Gly	Thr	Pro	Glu	Gln	Gly
									25						30
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
									40						45
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
									55						60
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
									70						80
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
									85						95
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
									100						110
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
									115						125
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
									130						140
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
									145						160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
									165						175
Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Pro	Met	Phe	
									180						190
Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	Ser	Asn	Thr	Glu	Leu	Gly	Ile
									195						205
Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr	Pro	Ile	Ala	Phe	Ala	Arg	Ser
									210						220
Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val	Asp	Gly	Thr	Ala	Gly	Pro	Gly
									225						240
Ser	Ala	Ala	Thr	Leu	Asp	His	Asn	Gln	Pro	Tyr	His	Ile	Cys	Arg	Gly
									245						255
Phe	Thr	Cys	Phe	Lys	Lys	Pro	Pro	Thr	Pro	Pro	Pro	Glu	Pro	Glu	Thr
									260						270

<210> 27

<211> 840

<212> DNA

<213> Artificial sequence
 <220>
 <223> nucleic acid sequence for the CopGFP-NA3 variant
 <400> 27
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 ctgaacggcg tggagttcga gctgggtggc ggcggagagg gcaccccccga gcagggccgc 120
 atgaccaaca agatgaagag caccaagggc gccctgacct tcagcccccta cctgctgagc 180
 cacgtatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc 240
 ttccctgcacg ccatcaacaa cggcggctac accaacaccc gcatcgagaa gtacgaggac 300
 ggcggcgtgc tgacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgcac 360
 ttcaagggtgg tgggcacccgg cttcccccggag gacagcgtga tcttcaccga caagatcatc 420
 cgcagcaacg ccaccgtgga gcacctgcac cccatggcgc ataacgtgct ggtgggcagc 480
 ttcgccccca ccttcagcct ggcgcacggc ggctactaca gcttcgtggc ggacagccac 540
 atgcacttca agagcgccat ccaccccaagc atcctgcaga acggggggccc catgttcgcc 600
 ttccggccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac 660
 gccttcaaga ccccgatcgc attcggcaga tccagagccc aggccagcaa ctccggcgtg 720
 gatggcacag cgggaccggg atcggccgcg actctagatc ataatcagcc ataccacatt 780
 tgttagaggtt ttacttgctt taaaaaacct cccacacccctc cccctgaacc tgaaacataa 840

<210> 28
 <211> 279
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> amino acid sequence for the CopGFP-NA3 variant
 <400> 28

Met	Glu	Ser	Asp	Glu	Ser	Gly	Leu	Pro	Ala	Met	Glu	Ile	Glu	Cys	Arg
1										10				15	
Ile	Thr	Gly	Thr	Leu	Asn	Gly	Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly
										25				30	
Glu	Gly	Thr	Pro	Glu	Gln	Gly	Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr
								35		40			45		
Lys	Gly	Ala	Leu	Thr	Phe	Ser	Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly
								50		55			60		
Tyr	Gly	Phe	Tyr	His	Phe	Gly	Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro
								65		70			75		80
Phe	Leu	His	Ala	Ile	Asn	Asn	Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu
								85		90			95		
Lys	Tyr	Glu	Asp	Gly	Gly	Val	Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr
								100		105			110		

Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
115 120 125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
130 135 140

Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145 150 155 160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
165 170 175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
180 185 190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
195 200 205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
210 215 220
Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val
225 230 235 240
Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln
245 250 255
Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr
260 265 270
Pro Pro Pro Glu Pro Glu Thr
275